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Short communication

Title

Hunting the hunter: using genetic profiling for improved management of shark attacks on humans

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Summary

DNA evidence is routinely used to identify individual predators responsible for attacks on people and livestock in terrestrial settings. However, the use of transfer DNA techniques in aquatic environments for similar purposes is a recent development. To date, DNA barcoding has been used successfully to identify shark species depredating fish catches and biting surfboards and neoprene surfaces. In this study we demonstrate the successful DNA barcoding and fingerprinting of individual sharks from transfer DNA collected directly from the wounds of two shark bite victims. The successful use of DNA techniques to identify both species and specific individuals responsible for shark bites opens the door to selective removal of these individuals as an innovative shark bite risk management strategy. This selective approach would be a more effective, eco-responsible, cost-effective and ethical solution for vulnerable taxa than ongoing non-selective culling campaigns.

Introduction

Recent decades have seen the adoption of DNA forensic techniques for solving wildlife poaching cases and identifying culprits in terrestrial predator attacks on humans^{1,2}. Analysis of mitochondrial DNA (mtDNA ‘barcoding’) is used to identify species³, whereas analysis of nuclear DNA (nDNA ‘fingerprinting’) can distinguish between individuals of the same species⁴. Microsatellites (short tandem repeats, STRs) are the preferred nuclear markers for DNA fingerprinting because of their polymorphic and co-dominant nature, strict adherence to Mendelian inheritance and high reproducibility⁵. STRs have been used to solving poaching cases involving wild boar⁶ and Sardinian Mouflons^{7,8}, and to identify individual brown bears (*Ursus arctos*) and tigers (*Panthera tigris*) responsible for fatal attacks on humans^{9,10}. The source of DNA in these cases was either hair or blood, but successful DNA fingerprinting has also been achieved using saliva left in dog bite wounds on a child in Japan¹¹ and livestock in Italy¹². In these cases it was important to identify the specific "problem individual"^{13,14} responsible for the attack in order to eliminate the threat.

Shark bites on humans, commonly referred to as "shark attacks", cause about ten fatalities each year¹⁵ but receive extensive sensationalized media coverage leading to distorted public perceptions of risk¹⁶. This biased perception is reinforced by the existence of chronic clusters of bites in certain areas such as northeastern Brazil (Western Central Atlantic Ocean), Reunion Island (Indian Ocean) or the coasts of Australia, New Caledonia or Hawaii (Eastern Central Pacific)¹⁷. Common shark bite mitigation measures include the use of nets or repellent barriers to limit contact between ocean users and sharks¹⁸, early detection of the animals by human spotters¹⁹, drones²⁰ or telemetry²¹, and personal shark repellent devices^{22,23}. However, non-selective mass shark culling campaigns are also still used despite the lack of evidence for their effectiveness. Previous studies concluding that culling campaigns improve human safety^{24,25} lack appropriate controls and show apparent trends that may simply reflect the natural rarity and stochasticity of fatal bites on humans. Other studies have shown culling campaigns do not reduce shark bites²⁶. Indiscriminate culling of 174 tiger sharks and 125 bull sharks between January 2014 and November 2020 did not prevent the occurrence of six fatal bites around La Reunion Island (2,512 sq.km) during this period (an average of 1 fatality per year), compared to five

fatal bites between 2010 and 2013 (an average of 1.2 fatalities per year). Recreational ocean use around La Reunion Island has decreased significantly since 2014²⁷, suggesting shark bite risk may actually have increased during the period of culling. The effectiveness and ethical appropriateness of shark culling is increasingly criticized by scientists and the general public alike^{28,29,30}.

The rationale for mass shark culling is two-fold; (1) the culprit responsible for a bite incident may be among the sharks removed, and (2) reducing the density of sharks reduces shark bite risk. Reducing animal densities to mitigate problematic behaviors can be effective in cases where the majority of individuals are engaged in these behaviors, such as great cormorants (*Phalacrocorax carbo sinensis*) depredating fish catches³¹, sika deer (*Cervus nippon*) damaging trees³², or wild boar damaging crops³³. However, shark bites on humans are atypical behavior for sharks – they are very rare events despite high levels of human ocean recreation activities around the world. It is possible that problem individuals exist in shark populations just as they do in populations of terrestrial predators¹⁵ and shark bites result from the atypical behavior of a few such individuals. Sharks that bite people may be at the extreme end of the behavioral spectrum for traits such as boldness (vs. shyness) and risk taking (vs. avoidance)³⁴. If problem individuals exist in shark populations then they could be selectively removed following bite incidents to prevent future incidents, as is the case in terrestrial environments with large predators¹⁴. Genetic profiling could be used to unequivocally identify both the species and the individual responsible for bite incidents. However, this would be contingent on DNA persisting in bite wounds despite the potential for seawater to wash it away. Recent studies have successfully used transfer DNA recovered from depredated fish catches³⁵, neoprene and surfboards³⁶ to identify the culprit shark species. However, to date no study has identified both the shark species (via barcoding) and the individual within that species (via fingerprinting) using transfer DNA recovered directly from shark bite wounds in human flesh.

Here we demonstrate the successful use of transfer DNA recovered from the wounds of two recent shark bite victims to identify the culprit species and demonstrate that a different individual was responsible for each bite. We discuss the implications of DNA profiling for shark bite mitigation.

84 **Results**

85 Two swimmers were recently bitten by sharks in waters off St. Martin (French West-Indies) and the
86 neighboring island of Nevis (West-Indies). Both incidents were witnessed by observers that visually
87 identified the culprit as a tiger shark (*Galeocerdo cuvier*) in both cases. Medical personnel swabbed the
88 bite wounds within a few hours of each incident. We successfully recovered shark mitochondrial DNA
89 from these swabs and performed a barcoding analysis confirming the visual identification of a tiger
90 shark in each case. All six swabs collected from the St Kitts-and-Nevis incident matched reference tiger
91 shark mtDNA (4>98% match, 2>94% match). Five swab samples from St Martin yielded a >98% match
92 to *Galeocerdo cuvier* and one failed. The transfer DNA recovered from both victims also allowed the
93 fingerprinting of both shark individuals based on 25 composite short tandem repeats (STR) (see Table
94 S1). A comparison of the two individual genetic profiles showed that the two bites were perpetrated by
95 two different individuals (see Table S2). As these were first-time analyses, it took several weeks to
96 obtain results. With preparation, the waiting time for barcoding and fingerprinting results could be
97 reduced to an average of 36-40 hours and 5-7 days, respectively. Such delays would perfectly fit with
98 the inclusion of DNA profiling in a short and long terms innovative strategy of shark risk management
99 (Fig. 1).

(photo-ID or ID tag) (e). Stomach contents of sharks matching the culprit species and size would be examined via ultrasonography or physical eversion in order to identify potential human remains. In absence of remains, the animal would be released; in presence of human remains, the animal would be culled (f). The transfer DNA from the human wounds would also allow (g) the fingerprinting of the animal responsible for the bite. (g) Long-term measures would include routine collection of shark DNA profiles and ID tagging or photography via non-lethal fishing or diver surveys at specific monitoring sites to build a shark identification database. (h) If a culprit shark DNA profile matches a known individual in the database, that specific individual would be targeted for selective removal based on unique external characteristics (ID tag or photo).

Discussion

We successfully barcoded and fingerprinted shark transfer DNA samples collected by swabbing bite wounds in two separate incidents. The swabbing was performed by different individuals in each case, the samples were stored in 90° alcohol and a regular freezer prior to analysis and standard protocols for DNA extraction, amplification and sequencing were applied to obtain the identification results. These results demonstrate that transfer DNA analyses could be a standard component of the forensic analysis of shark bite incidents, and would complement existing wound analyses used to estimate the size of the shark involved.

The ability to identify individual culprits provides a potential alternative to mass-culling. Non-lethal fishing could be used to try and find the individual responsible. The stomach contents of captured sharks meeting the culprit species (determined via barcoding) and size criteria (within a +/-10% error) could be non-lethally examined using a portable ultrasound unit to scan for human remains (especially bones that are more resistant to digestive juices). Our successful fingerprinting of transfer DNA from bite wounds could allow the culprit to be definitively identified and selectively removed in a similar manner to terrestrial predators that kill humans. However, the concealing nature of the ocean and wide-ranging behavior of some large shark species makes this approach more challenging than in

terrestrial settings where large predators typically occupy well-defined home ranges, exhibit territoriality or defend carcasses and can be relatively easily found. Possible solutions to this considerable challenge include pre-emptively creating genetic reference databases of large sharks using non-lethal sampling methods (e.g. biopsy sampling of free-swimming or captured individuals). Following a severe shark bite incident, the fingerprint obtained from transfer DNA could be compared to the database to identify a specific culprit that would be externally identifiable from an identification tag or photo-ID. Once identified as responsible for a bite on humans and found again thanks to a monitoring sites, the problem individuals could be removed (Fig. 1).

Existing examples of animal genetic profile databases include brown bears (*Ursus arctos*) (n=479)³¹ and rhinoceros (species)(n>3,900). In Africa, the RhODIS® (Rhinoceros DNA Index System) database facilitated the criminal prosecution of several poachers via DNA matches between the database and confiscated material³⁷. Estimating shark population sizes is challenging and prone to large error margins but existing population size estimates (e.g. 1200 bull sharks around La Reunion island³⁸, 2,500–6,750 white sharks off Eastern Australia and New Zealand³⁹) illustrate the scale of sampling required to create genetic profile databases. Although shark species primarily responsible for biting humans may range over thousands of kilometers of ocean, they also return to specific locations within their home ranges. For example, satellite-tagged bull sharks and tiger sharks have moved over hundreds of kilometers in the Pacific⁴⁰ and thousands of kms in the Western Atlantic⁴¹, respectively, before returning to artificial provisioning sites.

Selective approaches have the potential to be less costly than existing culling campaigns. La Reunion island had a 2018 annual budget of 2.2 million USD for shark bite risk management, including 660.000 USD for shark culling. Eighty (65 tiger and 15 bull) sharks were culled at a cost of US\$8,250 per shark, but two fatal bites still occurred in January and May 2019³⁰. Creating a La Reunion shark DNA fingerprint database (using 20-loci as for the present study) would cost of 660.000 USD based on the current shark population size estimate and analysis costs of US\$40-50 per shark. The field

sampling (i.e. fishing) costs would be comparable to those for the lethal culling campaign and would be spread over several years.

The substantially lower ecological impact of selective shark removal compared to mass culling should also be weighed in the cost-benefit analysis. Shark populations are already severely overfished in many locations around the world⁴². The removal of large numbers of top level predators reduces population genetic diversity and may result in undesirable cascade effects through marine food webs. Similar negative impacts may result from large scale shark culling. Selective removal of a small number of sharks known to have bitten humans would bring shark bite mitigation in line with the management of terrestrial predators responsible for targeting humans.

Material and methods

DNA extraction and sequencing

DNA was extracted from the swab tips from St Martin (n=6 swabs) and St Kitts-and-Nevis (n=6 swabs) using the Gentra Puregene DNA Purification Kit (Qiagen) following manufacturer instructions. DNA extraction quality was visualized on a 2% agarose gel.

Taxonomic identification was performed using the 260 bp CO1shark25F – CO1shark315R fragment (CO1shark25F -5' AGCAGGTATAGTTGGAACAGCCC 3' and CO1shark 315R -5' GCTCCAGCTTCTACTCCAGC 3') (Fotedar et al., 2019). Mitochondrial sequences were amplified using Quiagen reagents kit (preciser), with 2.5µl Tampon TAQ 10X, 2µl MgCl2 25 mM, 2.5µl dNTPs 2 mM, 0.6µl of each primer (10µM), 0.1µl Taq polymerase (5u/µl), Ultra Pure H2O, 5µl QSolution, for a final volume of 25µl. PCR programs consisted of an initial denaturing step at 95 °C for 3 min., followed by 35 cycles of 95 °C for 30 sec, 62 °C for 45 sec, and 72 °C for 30 sec, finished by 10 min at 72 °C and then held at 4°C (Thermocycler Eppendorf nexus gradient). PCR products were all ran on a 2 % agarose gel. PCR products were sequenced by GenoScreen (Lille – France) using an Applied Biosystem's 3730xl DNA Analyzer.

Sequence data were analyzed with BioEdit 7.2.5 and exported to the BLAST function (fasta format) from GenBank. CO1shark25F – CO1shark315R sequences were assigned allowing a best match score > 98%.

Genomic DNA Microsatellite markers were amplified using Type-it Microsatellite PCR kit (Qiagen, Hilden, Germany) in a final volume of 10 µL including 5 µL Type-it Multiplex PCR Master Mix (2X), 0.04 µL of each primer (25 µM forward and reverse primers diluted in TE pH 8 buffer) and 1 µL of DNA. PCR programs consisted of an initial denaturing step of 15 min at 95 °C, followed by 40 cycles of 1 min at 95 °C, 1 min at specified annealing temperature (53°C, 56° or 58°C – see Table S1), 72 °C for 1 min, and a final elongation step at 72°C for 20 min. Due to the very low genomic DNA quantity, all loci were amplified in Monoplex, PCR products were sequenced by GenoScreen (Lille – France) using an Applied Biosystems 3730 Sequencer. GeneScan 500 LIZ (Applied Biosystems) was used for accurate sizing. Allele sizes were scored and checked manually using GENEMAPPER 3.7 (Applied Biosystems).

REFERENCES

1. Alacs, E. A. et al. DNA detective: a review of molecular approaches to wildlife forensics. *Forensic Sci Med Pathol.* **6**(3),180-194 (2010).
2. Arenas, M. et al. Forensic genetics and genomics: Much more than just a human affair. *PLoS Genet* **13**(9), e1006960 (2017).
3. Hebert, P. D., Ratnasingham, S. & deWaard, J. R. Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. *Proc Biol Sci.* **270** Suppl 1:S96±9 (2003).
4. Jeffreys, A., Wilson, V. & Thein, S. Hypervariable ‘minisatellite’ regions in human DNA. *Nature* **314**, 67–73 (1985).
5. Singh, A. et al. A novel microsatellite (STR) marker for forensic identification of big cats in India. *Forensic Sci Int.* **141**(2±3), 143±7 (2004).
6. Lorenzini, R. DNA forensics and the poaching of wildlife in Italy: a case study. *Forensic Sci Int.* **153**(2±3), 218±21 (2005).

7. Lorenzini, R. et al. Wildlife molecular forensics: identification of the Sardinian mouflon using STR profiling and the Bayesian assignment test. *Forensic Sci Int Genet.* **5**(4), 345±9 (2011).
8. Barbanera, F. et al.. Conservation of endemic and threatened wildlife: molecular forensic DNA against poaching of the Cypriot mouflon (*Ovis orientalis ophion*, Bovidae). *Forensic Sci Int Genet.* **6**(5), 671±5 (2012).
9. Frosch, C. et al. Case report of a fatal bear attack documented by forensic wildlife genetics. *Forensic Sci Int Genet.* **5**(4), 342-344 (2011).
10. Lorenzini R. DNA forensics and the poaching of wildlife in Italy: a case study. *Forensic Sci Int.* **153**(2±3):218±21 (2005).
11. Tsuji, A. et al. Unusual death of a baby: a dog attack and confirmation using human and canine STRs. *Int J Legal Med.* **122**(1), 59±62 (2008).
12. Caniglia, R., et al. Who is who? Identification of livestock predators using forensic genetic approaches. *Forensic Sci Int Genet.* **7**(3), 397-404 (2013).
13. Linnell, J. D. et al. Large carnivores that kill livestock: do "problem individuals" really exist?. *Wildlife Soc. Bul.*, 698-705 (1999).
14. Swan, G. J. et al. Ecology of problem individuals and the efficacy of selective wildlife management. *Trends in Ecol & Evol* **32**(7), 518-530 (2017).
15. Clua, E. E., & Linnell, J. D. Individual shark profiling: An innovative and environmentally responsible approach for selectively managing human fatalities. *Cons Lett* **12**(2), e12612 (2019).
16. Pepin-Neff, C., & Wynter, T. Save the sharks: reevaluating and (re) valuing feared predators. *Hum Dim of Wildlife* **24**(1), 87-94 (2019).
17. Chapman, B. K. & McPhee, D. Global shark attack hotspots: Identifying underlying factors behind increased unprovoked shark bite incidence. *Oc & Coast Manag*, **133**, 72-84 (2016).
18. O'Connell, C. P., et al. Testing the exclusion capabilities and durability of the Sharksafe Barrier to determine its viability as an eco-friendly alternative to current shark culling methodologies. *Aqu Cons: Mar and Freshwater Ecosyst*, **28**(1), 252-258 (2018).

19. Curtis, T. H. et al. Responding to the risk of White Shark attack. Global Perspectives on the Biology and Life History of the White Shark. CRC Press, 477-510 (2012).
20. Butcher, P. A. et al. Beach safety: can drones provide a platform for sighting sharks?. *Wild Res* **46**(8), 701-712 (2020).
21. Meeuwig, J. J. & Ferreira, L. C. Moving beyond lethal programs for shark hazard mitigation. *An Cons*, 17(4), 297-298 (2014).
22. Huveneers, C. et al. Effectiveness of five personal shark-bite deterrents for surfers. *PeerJ* **6**, e5554 (2018).
23. Whitmarsh, S. K. et al. Effectiveness of novel fabrics to resist punctures and lacerations from white shark (*Carcharodon carcharias*): Implications to reduce injuries from shark bites. *PloS one* **14**(11), e0224432 (2019).
24. Dudley, S. F. J. A comparison of the shark control programs of New South Wales and Queensland (Australia) and KwaZulu-Natal (South Africa). *Oc & coast manag* **34**(1), 1-27 (1997).
25. Cliff, G. & Dudley, S. F. Reducing the environmental impact of shark-control programs: a case study from KwaZulu-Natal, South Africa. *Mar and Fresh Res* **62**(6), 700-709 (2011).
26. Wetherbee, B., Lowe, C. & Crow, G. A review of shark control in Hawaii with recommendations for future research. *Pac Sci* **48**, 95–115 (1994).
27. Lagabrielle, E. et al. Environmental and anthropogenic factors affecting the increasing occurrence of shark-human interactions around a fast-developing Indian Ocean island. *Sci rep* **8**(1), 1-13 (2018).
28. Gross, M. Learning to live with sharks. *Science* R341 (1994).
29. Ferretti, F. et al. Reconciling predator conservation with public safety. *Front in Ecol and Env* **13**(8), 412-417 (2015).
30. Clua, E. E. et al. Selective removal of problem individuals as an environmentally responsible approach for managing shark bites on humans. *Oc & Coast Manag* **194**, 105266 (2020).
31. Andreassen, R. et al. A forensic DNA profiling system for Northern European brown bears (*Ursus arctos*). *For Sci Int: Gen* **6**(6), 798-809 (2012).

32. Ueno, M., Kaji, K. & Saitoh, T. Culling versus density effects in management of a deer population. *J of Wild Manag* **74**(7), 1472-1483 (2010).
33. Croft, S., Franzetti, B., Gill, R. & Massei, G. Too many wild boar? Modelling fertility control and culling to reduce wild boar numbers in isolated populations. *PloS one* **15**(9), e0238429 (2020).
34. Réale, D. et al. Integrating animal temperament within ecology and evolution. *Biol rev* **82**(2), 291-318 (2007).
35. Fotedar, S. et al. Molecular tools for identification of shark species involved in depredation incidents in Western Australian fisheries. *PloS one* **14**(1), e0210500 (2019).
36. Kraft, D. et al. Development and successful real-world use of a transfer DNA technique to identify culprit species in shark bite incidents. *J For Sci* (In press).
37. Harper, C. et al. Robust forensic matching of confiscated horns to individual poached African rhinoceros. *Cur Biol* **28**(1), R13-R14 (2018).
38. CHARC. Etude du comportement des requins bouledogue (*Carcharhinus leucas*) et tigre (*Galeocerdo cuvier*) à La Réunion. RAPPORT SCIENTIFIQUE FINAL DU PROGRAMME CHARC (Connaissances de l'écologie et de l'Habitat de deux espèces de Requins Côtiers sur la côte ouest de La Réunion). 130 pp. 2015.
39. Hillary, R. et al. Genetic relatedness reveals total population size of white sharks in eastern Australia and New Zealand. *Sci rep* **8**(1), 1-9 (2018).
40. Brunnschweiler, J. M., Queiroz, N. & Sims, D. W. Oceans apart? Short-term movements and behaviour of adult bull sharks *Carcharhinus leucas* in Atlantic and Pacific Oceans determined from pop-off satellite archival tagging. *J fish biol* **77**(6), 1343-1358 (2010).
41. Hammerschlag, N. et al. Don't bite the hand that feeds: assessing ecological impacts of provisioning ecotourism on an apex marine predator. *Funct Ecol* **26**(3), 567-576 (2012).
42. Pacoureau, N. et al. Half a century of global decline in oceanic sharks and rays. *Nature* **589**(7843), 567-571 (2021).

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Author contributions

E.C. was the Coordinator of the project, and conceived the project together with S.P., C.M., J.L., A.H. and T.V. M.V. was involved in supervising the DNA sampling, storage and transportation. S.B. conducted the barcoding and fingerprinting analysis and forensic validation under S.P. supervision. The genetic data analyses were carried out by S.P.T.V. provided overall input to the paper as external experts. E.C. drafted the paper that was improved and accepted by all co-authors.

Supplementary material

S1: Table S1 Genetic characterization of twenty-two microsatellite loci in tiger shark (*Galeocerdo cuvier*)

S2: Table S2 Fingerprinting unmatching based on comparison of STRs from both sharks.

Additional information

Supplementary Information accompanies this paper at <http://www>.

Competing financial interests: The authors declare no competing financial interests. Reprints and permission information is available online at <http://>

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [S1Table1STR.pdf](#)
- [S2Table2fingerprintingunmatching.pdf](#)